



SEQUENCE LISTING

1

<110> Callen, Walter
Richardson, Toby
Frey, Gerhard
Miller, Carl
Kazaoka, Martin
Short, Jay
Mathur, Eric

<120> ENZYME HAVING ALPHA AMYLASE ACTIVITY
AND METHODS OF USE THEREOF

<130> 09010-107001

<140> 10/081,739
<141> 2002-02-21

<150> 60/270,495
<151> 2001-02-21

<150> 60/270,496
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<150> 60/291,122
<151> 2001-05-14

<160> 69

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated

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gccggaatct ccgcaatatg gattcccccg gcgagcaagg gcatggcgcc cgccatttcg 180
atgggctacg acccctacga ctctttgac ctcggtgagt acgaccagaa gggAACGGTA 240
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tggctcaaca aggataagct caagaacctc atctggatac atgagaacct cgccggagga	1020
agcaccgaca tagtctacta cgataacgt gaactcatct tcgtcaggaa cggctacggg	1080
gacaagccgg ggcttataac ctacatcaac ctaggtcga gcaaggccgg aaggtgggtt	1140
tatgtgccga agttcgccgg cgcgtgcatt cacgagtata ctggtaacct cggaggctgg	1200
gttagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct	1260
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<212> PRT
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<220>
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Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile	
35 40 45	
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp	
50 55 60	
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val	
65 70 75 80	
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr	
85 90 95	
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His	
100 105 110	
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr	
115 120 125	
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr	
130 135 140	
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe	
145 150 155 160	
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp	
165 170 175	
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly	
180 185 190	
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val	
195 200 205	
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr	
210 215 220	
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly	
225 230 235 240	
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe	
245 250 255	
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln	
260 265 270	
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn	
275 280 285	
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile	
290 295 300	
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu	
305 310 315 320	
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Glu Asn	

325	330	335	
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu			
340	345	350	
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr			
355	360	365	
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys			
370	375	380	
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp			
385	390	395	400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro			
405	410	415	
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr			
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Cys Gly Val Gly			
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<210> 3

<211> 1419

<212> DNA

<213> Environmental

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gatggcacgt tatggaccaa agtgccaat gaagccaaca acttatccag ccttggcatc	180
accgctctt ggctgcgccc cgcttacaaa ggaacaagcc gcagcgcacgt agggtacgga	240
gtatacact tggatgacct cgccgaattt aatcaaaaag ggaccgtccg cacaataac	300
gaaacaaaag ctcaatatct tcaagccatt caagccccc acgcccgtgg aatgcacgtg	360
tacggcgatg tcgtgttcga ccataaaggc ggcgctgacg gcacggatg gttggacgccc	420
gtcgaagtca atccgtccga ccgcaaccaa gaaatctgg gcacctatca aatccaagca	480
tggacgaaat ttgattttcc cggggggggg aacacctact ccagctttaa gtggcgctgg	540
taccattttgc acggcggttga ttgggacgaa agccgaaaat tgagccgcat ttacaaattc	600
cgcggcatcg gcaaagcgtg ggattggaa gtagacacgg aaaacggaaa ctatgactac	660
ttaatgtatg ccgaccttga tatggatcat cccgaagtgc tgaccgagct gaaaaactgg	720
ggggaaatggt atgtcaacac aacgaacatt gatgggttcc ggcttgcgtgc cgtcaagcat	780
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ctatttaccg tcggggataa ttggagctat gacatcaaca agttgcacaaa ttacattacg	900
aaaacagacg gaacgatgtc ttgtttgtat gccccgttac acaacaaatt ttataccgt	960
tccaaatcag ggggcgcatt tgatatgcgc acgtaatga ccaataactct catgaaagat	1020
caaccgcacat tggccgtcac ctcgttgcatt aatcatgaca ccgaacccgg ccaagcgctg	1080
cagtcatggg tcgaccatg gtcacaaaccg ttggcttacg cctttattct aactcggcag	1140
gaaggatacc cgtgcgtctt ttatggtgac tattatggca ttccacaata taacattcct	1200
tcgctgaaaa gcaaaatcga tccgctcctc atcgccgcga gggattatgc ttacggaacg	1260
caacatgatt atcttgcata ctcgcacatc atcgggtgga caagggaaagg ggtcactgaa	1320
aaaccaggat ccgggctggc cgcactgatc accgatgggc cgggaggaag caaatggatg	1380
tactgttggc aaacaacacg ctggaaaagt gttctatga	1419

<210> 4

<211> 1539

<212> DNA

<213> Environmental

<400> 4

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gaatggataca tgcccaatga cggccaaacat tggaagcgc tgcaaaacgca ctcggcatat	180
ttggctgaac acggattttac tgccgtctgg attccccgg catataaggg aacgagccaa	240

gcggatgtgg	gctacggtgc	ttacgacctt	tatgatttag	gggagttca	tcaaaaagg	300			
acgggtcgga	caaagtacgg	caca	aaaagga	gagctgcaat	ctgcgatcaa	aagtcttc	360		
tcccgcaca	ttaacgttta	cgggatgtg	gtc	atcaacc	aca	aaaggcgg	420		
acccaagatg	taaccgcgg	tga	agtcgat	cccgctgacc	gca	accgcgt	480		
gaacaccgaa	ttaaaggctg	gacacat	ttt	cat	ttccgg	ggcgcggcag	540		
gattttaaat	ggcatttgta	ccat	tttgac	ggaaccgatt	gggacgagtc	ccgaaagctg	600		
aaccgcac	ataagttca	aga	aaaggct	tgggattggg	aagt	ttccaa	tgaaaacgg	660	
aactatgatt	atttgatgt	tgcc	gacatc	gattatgacc	atc	cgtatgt	cgcagcagaa	720	
attaagagat	ggggcactt	gtat	gccaat	gaactgcaat	tgg	acgggtt	ccgtctt	780	
gctgtcaaa	acatta	aaatt	ttcttttt	cgggattggg	ttaat	catgt	caggaaaaaa	840	
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aactattga	acaaaacaaa	ttt	aatcat	tcagttt	acgt	ccgcgt	tcattat	960	
ttccatgt	catcgacaca	ggg	aggcggc	tatgat	gaa	attgct	gaacggtac	1020	
gtcg	ttt	cca	agcatcg	gaa	acg	gggtt	acat	tttgc	1080
ggc	aat	tcg	ttt	caaa	tgg	ttt	aaac	tttgc	1140
ctcaca	agg	aaat	ctggata	ccct	cagg	ttt	tttgc	tttgc	1200
gact	ccc	cag	gc	ttt	tttgc	tttgc	tttgc	tttgc	1260
aaac	acgt	atg	cg	tttgc	tttgc	tttgc	tttgc	tttgc	1320
aca	agg	gg	gac	tttgc	tttgc	tttgc	tttgc	tttgc	1380
ccc	gg	gg	gac	tttgc	tttgc	tttgc	tttgc	tttgc	1440
attac	ccg	gaa	acc	tttgc	tttgc	tttgc	tttgc	tttgc	1500
gttac	ggc	ggc	gtt	tttgc	tttgc	tttgc	tttgc	tttgc	1539

<210> 5

<211> 1395

<212> DNA

<213> Environmental

<400> 5

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atgc	agg	cct	tct	ccgg	tgt	ccc	ggg	ggg	180
aaa	atc	ccg	act	ggg	ttt	ccg	ggg	ggg	240
ggg	atg	ggc	gtt	ggg	ccg	ccg	ggg	ggg	300
tac	ttt	ggg	ttt	ttt	ccg	ccg	ttt	ttt	360
ttt	atc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	420
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	480
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	540
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	600
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	660
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	720
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	780
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	840
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	900
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	960
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	1020
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	1080
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	1140
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	1200
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	1260
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	1320
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	1380
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	1440
ttt	cc	ggg	ttt	ttt	ccg	ccg	ttt	ttt	1500
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<210> 6

<211> 1386

<212> DNA

<213> Bacteria

<400> 6

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gccttctact	gggacgtccc	aggtggagga	atctgggg	acaccatcag	gagcaagata	180
ccggagtggt	acgaggccgg	aatatccgcc	atttggattc	cgcgcagccag	caaggggatg	240
agcggcggtt	actcgatggg	ctacgatccc	tacgatttct	ttgacctcg	cgagtacaac	300
cagaagggaa	ccatcgaaac	gcgcttggc	tctaaacagg	agctcatcaa	tatgataaac	360
acggcccatg	cctacggcat	aaaggtcata	gcccgcacatcg	tcataaaacca	ccgcgcaggc	420
ggagacctcg	agtggAACCC	gttcgttggg	gactacacct	ggacggactt	ctcaaagggt	480
gcctcgggca	aatatactgc	caactaccc	gacttccacc	ccaacgaggt	caagtgtgt	540
gacgagggca	catttggagg	cttcccagac	atagcccacg	agaagagctg	ggaccagcac	600
tggctctggg	cgagcgatga	gagctacgcc	gcctaccta	ggagcatcg	cggtatgcc	660
tggcgctttg	actacgtgaa	gggctacgg	gcgtgggtcg	tcaaggactg	gctcaactgg	720
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tcccgcgacc	cggtcaaggc	cgttaacctt	gtagcaaacc	acgacaccga	tataatctgg	960
aacaagtacc	ttgcttatgc	tttcatccctc	acctacgaag	gccagcccg	catattctac	1020
cgcgactacg	aggagtggct	caacaaggac	aggttgaaca	acctcatatg	gatacacgac	1080
caccccgccag	gtggaaagcac	gagcatagtc	tactacgaca	gcgcgcgat	gatcttcgtg	1140
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<210> 7

<211> 472

<212> PRT

<213> Environmental

<400> 7

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								20		25			30		
Tyr	Phe	Glu	Trp	Tyr	Leu	Pro	Asp	Asp	Gly	Thr	Leu	Trp	Thr	Lys	Val
								35		40			45		
Ala	Asn	Glu	Ala	Asn	Asn	Leu	Ser	Ser	Leu	Gly	Ile	Thr	Ala	Leu	Trp
								50		55			60		
Leu	Pro	Pro	Ala	Tyr	Lys	Gly	Thr	Ser	Arg	Ser	Asp	Val	Gly	Tyr	Gly
							65		70			75			80
Val	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val
							85		90			95			
Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Ala	Gln	Tyr	Leu	Gln	Ala	Ile	Gln	Ala
							100		105			110			
Ala	His	Ala	Ala	Gly	Met	Gln	Val	Tyr	Ala	Asp	Val	Val	Phe	Asp	His
							115		120			125			
Lys	Gly	Gly	Ala	Asp	Gly	Thr	Glu	Trp	Val	Asp	Ala	Val	Glu	Val	Asn
							130		135			140			
Pro	Ser	Asp	Arg	Asn	Gln	Glu	Ile	Ser	Gly	Thr	Tyr	Gln	Ile	Gln	Ala
							145		150			155			160
Trp	Thr	Lys	Phe	Asp	Phe	Pro	Gly	Arg	Gly	Asn	Thr	Tyr	Ser	Ser	Phe
							165		170			175			
Lys	Trp	Arg	Trp	Tyr	His	Phe	Asp	Gly	Val	Asp	Trp	Asp	Glu	Ser	Arg

180	185	190
Lys Leu Ser Arg Ile Tyr Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp		
195	200	205
Trp Glu Val Asp Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala		
210	215	220
Asp Leu Asp Met Asp His Pro Glu Val Val Thr Glu Leu Lys Asn Trp		
225	230	235
Gly Lys Trp Tyr Val Asn Thr Asn Ile Asp Gly Phe Arg Leu Asp		
245	250	255
Ala Val Lys His Ile Lys Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr		
260	265	270
Val Arg Ser Gln Thr Gly Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp		
275	280	285
Ser Tyr Asp Ile Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asp Gly		
290	295	300
Thr Met Ser Leu Phe Asp Ala Pro Leu His Asn Lys Phe Tyr Thr Ala		
305	310	315
Ser Lys Ser Gly Gly Ala Phe Asp Met Arg Thr Leu Met Thr Asn Thr		
325	330	335
Leu Met Lys Asp Gln Pro Thr Leu Ala Val Thr Phe Val Asp Asn His		
340	345	350
Asp Thr Glu Pro Gly Gln Ala Leu Gln Ser Trp Val Asp Pro Trp Phe		
355	360	365
Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro		
370	375	380
Cys Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro		
385	390	395
Ser Leu Lys Ser Lys Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr		
405	410	415
Ala Tyr Gly Thr Gln His Asp Tyr Leu Asp His Ser Asp Ile Ile Gly		
420	425	430
Trp Thr Arg Glu Gly Val Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala		
435	440	445
Leu Ile Thr Asp Gly Pro Gly Ser Lys Trp Met Tyr Cys Trp Gln		
450	455	460
Thr Thr Arg Trp Lys Ser Val Leu		
465	470	

<210> 8

<211> 512

<212> PRT

<213> Environmental

<400> 8

Met Lys Gln Gln Lys Arg Leu Tyr Ala Arg Leu Leu Thr Leu Leu Phe			
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20	25	30	
Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro Asn Asp Gly			
35	40	45	
Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu Ala Glu His			
50	55	60	
Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln			
65	70	75	80
Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe			
85	90	95	
His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu Leu			

100	105	110
Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr Gly		
115	120	125
Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp Val		
130	135	140
Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser Gly		
145	150	155
Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg Gly		
165	170	175
Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Thr		
180	185	190
Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln Gly		
195	200	205
Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp Tyr		
210	215	220
Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala Glu		
225	230	235
Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp Gly		
245	250	255
Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg Asp		
260	265	270
Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr Val		
275	280	285
Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu Asn		
290	295	300
Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr Gln		
305	310	315
Phe His Ala Ala Ser Thr Gln Gly Gly Tyr Asp Met Arg Lys Leu		
325	330	335
Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr Phe		
340	345	350
Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr Val		
355	360	365
Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Glu		
370	375	380
Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys Gly		
385	390	395
Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro Ile		
405	410	415
Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr Phe		
420	425	430
Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser Val		
435	440	445
Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ala		
450	455	460
Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His Asp		
465	470	475
Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly Trp		
485	490	495
Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln Arg		
500	505	510

<210> 9
<211> 464
<212> PRT
<213> Environmental

<400> 9

Val Val His Met Lys Leu Lys Tyr Leu Ala Leu Val Leu Leu Ala Val
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 Glu Leu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val
 35 40 45
 Pro Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln Lys Ile Pro Glu
 50 55 60
 Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys
 65 70 75 80
 Gly Met Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe
 85 90 95
 Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe Gly
 100 105 110
 Ser Lys Glu Glu Leu Val Asn Met Ile Asn Thr Ala His Ser Tyr Gly
 115 120 125
 Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp
 130 135 140
 Leu Glu Trp Asn Pro Phe Val Asn Asn Tyr Thr Trp Thr Asp Phe Ser
 145 150 155 160
 Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro
 165 170 175
 Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Asp Phe Pro Asp
 180 185 190
 Ile Ala His Glu Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser Asn
 195 200 205
 Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile Asp Ala Trp Arg
 210 215 220
 Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Asn Asp Trp Leu
 225 230 235 240
 Ser Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val
 245 250 255
 Asp Ala Leu Leu Asn Trp Ala Tyr Asp Ser Gly Ala Lys Val Phe Asp
 260 265 270
 Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Thr Asn Ile
 275 280 285
 Pro Ala Leu Val Tyr Ala Leu Gln Asn Gly Gly Thr Val Val Ser Arg
 290 295 300
 Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile
 305 310 315 320
 Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly
 325 330 335
 Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp
 340 345 350
 Lys Leu Asn Asn Leu Ile Trp Ile His Glu His Leu Ala Gly Gly Ser
 355 360 365
 Thr Lys Ile Leu Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Met Arg Glu
 370 375 380
 Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Asn
 385 390 395 400
 Asp Trp Ala Glu Arg Trp Val Asn Val Gly Ser Lys Phe Ala Gly Tyr
 405 410 415
 Thr Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Arg Trp
 420 425 430
 Val Gln Tyr Asp Gly Trp Val Lys Leu Thr Ala Pro Pro His Asp Pro
 435 440 445

Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr Ala Gly Val Gly
 450 455 460

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<211> 461
<212> PRT
<213> Bacteria

<400> 10
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Glu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Gly
 35 40 45
Gly Gly Ile Trp Trp Asp Thr Ile Arg Ser Lys Ile Pro Glu Trp Tyr
 50 55 60
Glu Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met
 65 70 75 80
Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu
 85 90 95
Gly Glu Tyr Asn Gln Lys Gly Thr Ile Glu Thr Arg Phe Gly Ser Lys
 100 105 110
Gln Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys
 115 120 125
Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Asp Leu Glu
 130 135 140
Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val
 145 150 155 160
Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu
 165 170 175
Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala
 180 185 190
His Glu Lys Ser Trp Asp Gln His Trp Leu Trp Ala Ser Asp Glu Ser
 195 200 205
Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp
 210 215 220
Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asn Trp
 225 230 235 240
Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala
 245 250 255
Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe Asp Phe Pro
 260 265 270
Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Lys Asn Ile Pro Ala
 275 280 285
Leu Val Ser Ala Leu Gln Asn Gly Gln Thr Val Val Ser Arg Asp Pro
 290 295 300
Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp
 305 310 315 320
Asn Lys Tyr Leu Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro
 325 330 335
Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu
 340 345 350
Asn Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Ser
 355 360 365
Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile Phe Val Arg Asn Gly Tyr
 370 375 380

Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys
 385 390 395 400
 Val Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His
 405 410 415
 Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Tyr Val Tyr Ser
 420 425 430
 Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala Tyr Asp Pro Ala Asn Gly
 435 440 445
 Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
 450 455 460

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<220>
<223> Primer

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<220>
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<400> 13
gaaccgtctc aaaacacggc ccatgcctac ggc 33

<210> 14
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<210> 15
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gaacgtctca ggcgctttga ctacgtgaag ggc 33

<210> 16
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gaacggtctc aacaagatgg atgaggcatt tg 32

<210> 17
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<400> 17
gaaccgtctc acgatataat ctggaacaag taccttgc 38

<210> 18
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<400> 18
gaaccgtctc agaagcacga gcatagttta ctacg 35

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<400> 19
gaaccgtctc aaaggtgggt ttatgtgccg 30

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gaaccgtctc agaggttagtt ggcatatata ttg 33

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<400> 23
gaacgtctca cgccaggcat caacgccat g 31

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gaacgtctca ttgttagata gcggaaatgc 30

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<400> 25

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32

<210> 26

<211> 31

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<223> Primer

<400> 26

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31

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<211> 31

<212> DNA

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<223> Primer

<400> 27

gaaccgtctc accttccaac ctggctcgag c

31

<210> 28

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 28

tcgagactga ctctcaccca acaccgcaat agc

33

<210> 29

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 29

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50

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<400> 40
gaaccgtctc agaggttagtt ggccgtgtac ttg 33

<210> 41

<211> 30
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<220>
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<400> 41
gaacgtctca gccatgcgtc aacgcccgtg 30

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<400> 42
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<400> 43
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<210> 44
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<400> 44
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<400> 45
gaaccgtctc accttccggc ctggctcgag cc 32

<210> 46
<211> 35
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<220>

<223> Primer

<400> 46

tcgagactga ctctcagccc accccgcagt agctc

35

<210> 47

<211> 50

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<220>

<223> Primer

<400> 47

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50

<210> 48

<211> 30

<212> DNA

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<220>

<223> Primer

<400> 48

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<210> 49

<211> 31

<212> DNA

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<220>

<223> Primer

<400> 49

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31

<210> 50

<211> 33

<212> DNA

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<223> Primer

<400> 50

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33

<210> 51

<211> 31

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<220>
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<400> 51
gaacgtctca ggcgcttcga ctacgtcaag g 31

<210> 52
<211> 32
<212> DNA
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<220>
<223> Primer

<400> 52
gaacggtctc aacaagatgg acgaggcctt cg 32

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 53
gaaccgtctc acgatataat ctggaacaag 30

<210> 54
<211> 35
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<220>
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<400> 54
gaaccgtctc agaagcactg acatcgttta ctacg 35

<210> 55
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<400> 55
gaaccgtctc aaaggtgggt ttacgttccg 30

<210> 56
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<400> 56
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<220>
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<400> 57
gaacgggtctc agtttatcat gtttatgagc 30

<210> 58
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<400> 58
gaaccgtctc agaggttagtt ggccgtgtat ttac 34

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gaacgtctca cgccaggcat cgatgccgat 30

<210> 60
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gaacgtctca ttgttagaga gggcgaagtc aaag 34

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<212> DNA
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<220>
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<400> 61

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<212> DNA	
<213> Environmental	
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ggaatctggt gggacacgat agcccagaag atacccgact gggcaagcgc cgggatttcg	120
gcgatatgga tccctccgc gagcaagggt atgagcggcg gctattcgat gggctacgac	180
ccctacgatt attttgcacct rggtgagtac taccagaagg gaacqgtgga aacqaggttc	240
ggctcaaaggc aggagctcat aaacatgata aacaccgccc acgcctatgg catgaaggt	300

ata	gcccata	tagtcatcaa	ccaccgcgccc	ggcggtgacc	tggagtggaa	cccctcg	360
aac	gactata	cctggaccga	cttctcaaag	gtcgcgtcg	gtaaatacac	ggccaactac	420
ctc	gacttcc	acccgaacga	gctccatgcg	ggcgattccg	gaacatttg	aggctatccc	480
gac	atgc	atgc	acgacaagag	ctgggaccag	tactggctct	ggccagcca	540
gcg	catatc	tc	tcaggagcat	cgcatcgat	gcctggcgct	tcgactacgt	caagggctat
gtc	cccttgg	gg	tcgtcaagga	ctggctgaac	tggtggggag	gctggcggt	tggagagtac
tg	gacacca	ac	acgtcgacgc	tgttctcaac	tgggcatact	cgagcggtgc	caaggcttt
gac	tgc	cc	tctactaca	gatggacgag	gcctcgata	acaacaacat	tcccgcctg
gtg	gccc	cc	tcagatacgg	tcagacagt	gtcagccgcg	acccgttcaa	ggctgtgacg
ttt	tagcca	cc	accacgatac	cgacataatc	tggacaagt	atccagccta	cgcgttcatc
ctc	acctacg	cc	agggccagcc	gacaatattc	taccgcgact	acgaggagtg	gctcaacaag
gata	agctca	cc	agaacccat	ctggatacat	gacaacctcg	ccggagggag	cactgacatc
gtt	tactacg	cc	acaacgacga	gctgatattc	gtgagaaaacg	gctacggaag	caagccggga
ctg	ataacat	cc	acatcaac	ctgc	aaagccggaa	ggtgggtt	cgttccgaag
ttc	cgaggct	cc	cg	tgactaca	cgat	gcaatctcg	g
gtg	gactcaa	cc	g	cg	ggctgggt	ctac	ctcgag
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<210> 67

<211> 432

<212> PRT

<213> Environmental

<400> 67

Met	Ala	Leu	Glu	Glu	Gly	Ley	Ile	Met	Gln	Ala	Phe	Tyr	Trp	Asp	
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						20			25				30		
Asp	Trp	Ala	Ser	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Pro	Pro	Ala	Ser
						35			40				45		
Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly	Tyr	Asp	Pro	Tyr	Asp	Tyr
						50			55				60		
Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val	Glu	Thr	Arg	Phe
						65			70				75		80
Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr	Ala	His	Ala	Tyr
						85			90				95		
Gly	Met	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg	Ala	Gly	Gly
						100			105				110		
Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Asn	Asp	Tyr	Thr	Trp	Thr	Asp	Phe
						115			120				125		
Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr	Leu	Asp	Phe	His
						130			135				140		
Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly	Thr	Phe	Gly	Tyr	Pro	
						145			150				155		160
Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln	Tyr	Trp	Leu	Trp	Ala	Ser
						165			170				175		
Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly	Ile	Asp	Ala	Trp
						180			185				190		
Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Ala	Pro	Trp	Val	Val	Lys	Asp	Trp
						195			200				205		
Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr	Trp	Asp	Thr	Asn
						210			215				220		
Val	Asp	Ala	Val	Leu	Asn	Trp	Ala	Tyr	Ser	Ser	Gly	Ala	Lys	Val	Phe
						225			230				235		240
Asp	Phe	Ala	Leu	Tyr	Tyr	Lys	Met	Asp	Glu	Ala	Phe	Asp	Asn	Asn	
						245			250				255		
Ile	Pro	Ala	Leu	Val	Asp	Ala	Leu	Arg	Tyr	Gly	Gln	Thr	Val	Val	Ser

260	265	270
Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His	Asp Thr Asp	
275	280	285
Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu	Thr Tyr Glu	
290	295	300
Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu	Trp Leu Asn Lys	
305	310	315
Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu	Ala Gly Gly	
325	330	335
Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu Ile	Phe Val Arg	
340	345	350
Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile	Asn Leu Ala	
355	360	365
Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys Phe	Ala Gly Ser	
370	375	380
Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val	Asp Lys Trp	
385	390	395
Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala	His Asp Pro	
405	410	415
Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys	Gly Val Gly	
420	425	430

<210> 68

<211> 1386

<212> DNA

<213> Bacteria

<400> 68

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gcgttctact qggacgtgcc ttcaaggagga atatggtggg acacaatacg qcagaagata	180
ccggagtggt acgatgccgg aatctccgca atatggattc ccccccggcag caaggccatg	240
ggccggccct attcgatggg ctacgacccc tacgacttct ttgacctcgg tgagtacgac	300
cagaagggaa cggtagagac gcgccttggc tccaaggcagg agctcgtgaa catgataaac	360
accggcccacg cctacggcat caaggtcatc gcagacatag taatcaacca ccgcggccga	420
ggagaccttg agtggAACCC cttcgtcaat gactacacct ggacggactt ctcgaaggtc	480
gcttccggca agtacacggc caactacctc gacttccacc ccaacggaggta caagtgcgtc	540
gacggaggca cctttggagg gttccggac atagcccacg agaagagctg ggaccaggta	600
tggctctggg cgagcaacga gagctacgac gcctaccta ggagcatcgg cgttgacgca	660
tggcgcttcg actacgtcaa gggtacggc gcgtgggtcg tcaaggactg gctggactgg	720
tggggaggct gggccgtcgg ggagttactgg gacacaaaacg ttgatgcact gctcaactgg	780
gcctactcga gcgatgcaaa agtcttcgac ttcccgctct actacaagat ggacgccc	840
tttgcacaaca agaacattcc cgactcgac gaggccctca agaacggggg cacagtcgtc	900
agcccgccacc cggttaaggc cgtAACCTTC gttgcaaaacc acgacacggc cataattttgg	960
aacaagttacc cggcctacgc ctccatccctc acctacggc ggcagccgac gatattctac	1020
cgcgactacg aggaggggct caacaaggac aggctcaaga acctcatctg gatacacgac	1080
cacctcgccg gtggaaacgac cgacatagtc tactacgata acgatgaact catcttcgtc	1140
aggaacggct acggggacaa gccggggctt ataacctaca tcaacctagg ctcgagcaag	1200
gccggggagggt gggctacgt tccgaagttc gcgggagcgt gcatccacga gtacaccggc	1260
aacctcgccg gctgggtgga caagtgggtg gactcaagcg ggtgggtgt cctcgaggcc	1320
cctggcccacg acccgcccaa cggctattac ggctactccg tctggagcta ctgcggggtg	1380
ggctga	1386

<210> 69

<211> 461

<212> PRT

<213> Bacteria

<400> 69
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 Ala Gly Leu Tyr Ala Gln Pro Ala Gly Ala Ala Lys Tyr Leu Glu Leu
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 Glu Glu Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Ser
 35 40 45
 Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln Lys Ile Pro Glu Trp Tyr
 50 55 60
 Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met
 65 70 75 80
 Gly Gly Ala Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu
 85 90 95
 Gly Glu Tyr Asp Gln Lys Gly Thr Val Glu Thr Arg Phe Gly Ser Lys
 100 105 110
 Gln Glu Leu Val Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys
 115 120 125
 Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Asp Leu Glu
 130 135 140
 Trp Asn Pro Phe Val Asn Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val
 145 150 155 160
 Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu
 165 170 175
 Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala
 180 185 190
 His Glu Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser Asn Glu Ser
 195 200 205
 Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp
 210 215 220
 Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asp Trp
 225 230 235 240
 Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala
 245 250 255
 Leu Leu Asn Trp Ala Tyr Ser Ser Asp Ala Lys Val Phe Asp Phe Pro
 260 265 270
 Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp Asn Lys Asn Ile Pro Ala
 275 280 285
 Leu Val Glu Ala Leu Lys Asn Gly Gly Thr Val Val Ser Arg Asp Pro
 290 295 300
 Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp
 305 310 315 320
 Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro
 325 330 335
 Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu
 340 345 350
 Lys Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Asp
 355 360 365
 Ile Val Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Val Arg Asn Gly Tyr
 370 375 380
 Gly Asp Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys
 385 390 395 400
 Ala Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His
 405 410 415
 Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Trp Val Asp Ser
 420 425 430
 Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala His Asp Pro Ala Asn Gly

435 440 445
Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
450 455 460